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OM protein - protein search, using sw model

Run on: October 5, 2004, 11:24:28 ; Search time 13.8 Seconds

(without alignments)  
493.814 Million cell updates/sec

Title: US-09-840-795-15

Perfect score: 132

Sequence: 1 MDQQNEYWDQGRCVTCQR.....RPPTSXKXKXQQLIENGRX 132

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4.7	35.6	297	4 US-09-548-130-6	Sequence 6, Appli
2	4.7	35.6	299	4 US-09-548-110-2	Sequence 3, Appli
3	4.7	35.6	299	4 US-10-119-466-12	Sequence 12, Appli
4	7	5.3	577	4 US-09-107-532A-5217	Sequence 5217, Appli
5	7	5.3	857	4 US-08-187-554A-47	Sequence 47, Appli
6	7	5.3	857	4 US-09-527-431-47	Sequence 47, Appli
7	6	4.5	13	4 US-09-248-061B-15	Sequence 15, Appli
8	6	4.5	14	4 US-09-400-633A-36	Sequence 36, Appli
9	6	4.5	69	4 US-09-489-039A-7424	Sequence 7424, Appli
10	6	4.5	78	4 US-09-211-976-7280	Sequence 7280, Appli
11	6	4.5	124	4 US-09-107-532A-6397	Sequence 6397, Appli
12	6	4.5	159	4 US-09-732-210-184	Sequence 184, Appli
13	6	4.5	193	4 US-09-334-000C-3945	Sequence 3945, Appli
14	6	4.5	208	4 US-09-232-991A-1763B	Sequence 1763B, Appli
15	6	4.5	220	4 US-09-252-991A-2441	Sequence 26441, Appli
16	6	4.5	221	4 US-09-889-039A-10628	Sequence 10628, Appli
17	6	4.5	223	4 US-09-282-991A-20528	Sequence 20528, Appli
18	6	4.5	229	4 US-09-252-991A-28247	Sequence 29247, Appli
19	6	4.5	235	4 US-09-796-110-2	Sequence 2, Appli
20	6	4.5	238	4 US-09-334-000C-6030	Sequence 6030, Appli
21	6	4.5	250	3 US-09-167-717-2	Sequence 2, Appli
22	6	4.5	254	4 US-9-543-681A-6270	Sequence 6270, Appli
23	6	4.5	254	4 US-09-543-681A-6271	Sequence 6271, Appli
24	6	4.5	257	4 US-09-107-532A-5915	Sequence 5975, Appli
25	6	4.5	264	4 US-07-957-224B-34	Sequence 34, Appli
26	6	4.5	266	4 US-09-252-991A-2446	Sequence 27456, Appli
27	6	4.5	272	4 US-09-252-991A-20051	Sequence 20051, Appli

## ALIGNMENTS

RESULT 1  
US-09-548-130-6  
; Sequence 6, Application US/09548130  
; Patent No. 6534061  
; GENERAL INFORMATION:  
; APPLICANT: Godard, Audrey  
; APPLICANT: Pan, James  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND NUCLEIC ACIDS ENCODING THE SAME  
; FILE REFERENCE: P1739R1  
; CURRENT APPLICATION NUMBER: US/09/548-130  
; CURRENT FILING DATE: 2000-04-12  
; EARLIER APPLICATION NUMBER: US 60/112B, 849  
; EARLIER FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 6  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Human  
US-09-548-130-6

Query Match 35.6% ; Score 47; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 3.2e-39;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDQQNEYWDQGRCVTCQRCGPQELSKDCGYYGGDDAYCTACPBR 47

RESULT 2  
US-09-548-130-3  
; Sequence 3, Application US/09548130  
; Patent No. 6534061  
; GENERAL INFORMATION:  
; APPLICANT: Godard, Audrey  
; APPLICANT: Pan, James  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND NUCLEIC ACIDS ENCODING THE SAME  
; FILE REFERENCE: P1739R1  
; CURRENT APPLICATION NUMBER: US/09/548-130  
; CURRENT FILING DATE: 2000-04-12  
; EARLIER APPLICATION NUMBER: US 60/123B, 849  
; EARLIER FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 3  
; LENGTH: 299  
; TYPE: PRT

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2	56	72.7	299	4	US-09-548-130-3	Sequence 12, Appli
3	56	72.7	299	4	US-10-119-466-12	Sequence 20528, A
4	6	7.8	223	4	US-09-252-991A-20528	Sequence 18718, AP
5	6	7.8	266	4	US-09-543-681A-5038	Sequence 28595, A
6	6	7.8	275	4	US-09-252-991A-18717	Sequence 2, Appli
7	6	7.8	337	4	US-09-252-991A-28555	Sequence 25656, A
8	6	7.8	346	2	US-08-744-779A-2	Sequence 3444, AP
9	6	7.8	346	2	US-08-862-531-2	Sequence 13, Appli
10	6	7.8	356	4	US-09-252-991A-25656	Sequence 6660, AP
11	6	7.8	388	4	US-09-540-346-3444	Sequence 29544, A
12	6	7.8	393	4	US-09-194-905-13	Sequence 2, Appli
13	6	7.8	395	4	US-09-328-352-6660	Sequence 19593, A
14	6	7.8	420	4	US-09-252-991A-29544	Sequence 5452, AP
15	6	7.8	426	4	US-09-972-784-2	Sequence 27768, A
16	6	7.8	440	4	US-09-252-991A-19593	Sequence 8217, AP
17	6	7.8	443	4	US-09-543-681A-5452	Sequence 8519, AP
18	6	7.8	460	4	US-09-252-991A-27768	Sequence 22490, A
19	6	7.8	566	4	US-09-489-039A-8217	Sequence 13507, A
20	6	7.8	604	4	US-09-489-039A-8519	Sequence 29239, A
21	6	7.8	643	4	US-09-252-991A-22490	Sequence 4, Appli
22	6	7.8	686	4	US-09-489-039A-13507	Sequence 4, Appli
23	6	7.8	742	4	US-09-252-991A-29239	Sequence 4, Appli
24	6	7.8	746	4	US-09-543-681A-5452	Sequence 4, Appli
25	6	7.8	787	2	US-08-720-484A-4	Sequence 4, Appli
26	6	7.8	787	3	US-08-953-823A-4	Sequence 4, Appli
27	6	7.8	787	4	US-09-398-239-4	Sequence 4, Appli

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 5, 2004, 11:24:28 ; Search time 24.15 Seconds  
(without alignments)  
493.814 Million cell updates/sec

Title: US-09-840-795-19  
Sequence score: 231  
Sequence: 1 MDDCENYEWDQGRCVTCQRR.....AQLFSLDSVPFQQQQPEM 231

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgm2\_6/ptcdata/2/iaa/5B\_COMBO.PEP:  
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6: /cgm2\_6/ptcdata/2/iaa/backfile1.PEP:  
\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match %	Length	DB ID	Description
1	148	64.1	297	4	US-09-548-130-6	Sequence 6, Appli
2	115	49.8	299	4	US-09-548-300-3	Sequence 3, Appli
3	115	49.8	299	4	US-10-119-666-12	Sequence 12, Appli
4	8	3.5	151	3	US-09-286-529-4	Sequence 4, Appli
5	8	3.5	210	3	US-09-186-519-3	Sequence 3, Appli
6	8	3.5	487	4	US-09-328-552-6767	Sequence 677, Appli
7	8	3.5	626	2	US-08-596-000A-7	Sequence 7, Appli
8	8	3.5	626	2	US-08-596-300A-14	Sequence 14, Appli
9	7	3.0	121	2	US-08-134-555-9	Sequence 9, Appli
10	7	3.0	131	3	US-08-134-033A-10	Sequence 10, Appli
11	7	3.0	131	3	US-09-236-574-9	Sequence 9, Appli
12	7	3.0	131	4	US-09-363-226-9	Sequence 9, Appli
13	7	3.0	184	4	US-09-325-332A-16	Sequence 56, Appli
14	7	3.0	191	4	US-09-540-236-2276	Sequence 2276, Appli
15	7	3.0	197	4	US-09-480-397A-23	Sequence 23, Appli
16	7	3.0	197	4	US-09-747-259A-4	Sequence 4, Appli
17	7	3.0	197	4	US-09-816-744-4	Sequence 4, Appli
18	7	3.0	218	4	US-09-52-991A-18053	Sequence 18053, Appli
19	7	3.0	219	4	US-09-227-613-9	Sequence 19, Appli
20	7	3.0	228	4	US-09-252-991A-22217	Sequence 22217, Appli
21	7	3.0	247	4	US-09-489-039A-7332	Sequence 7332, Appli
22	7	3.0	259	4	US-09-252-991A-1664	Sequence 1664, Appli
23	7	3.0	287	4	US-09-439-261-13	Sequence 13, Appli
24	7	3.0	287	4	US-09-227-13-14	Sequence 14, Appli
25	7	3.0	288	4	US-09-439-261-14	Sequence 14, Appli
26	7	3.0	288	4	US-09-439-261-16	Sequence 16, Appli
27	7	3.0	288	4	US-09-439-261-18	Sequence 18, Appli

#### ALIGNMENTS

RESULT 1  
US-09-548-130-6  
; Sequence 6, Application US/09548130  
; Patent No. 653-061  
; GENERAL INFORMATION:  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOGS AND NUCLEIC ACIDS ENCODING THE SAME  
; FILE REFERENCE: P1739RI  
; CURRENT APPLICATION NUMBER: US/09-548-130  
; CURRENT FILING DATE: 2000-04-12  
; EARLIER APPLICATION NUMBER: US 60/128,849  
; EARLIER FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO: 6  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Human  
US-09-548-130-6

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Best Local Similarity 100.0%; Pred. No. 3e-39;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query 118 CAFQLSLVEAAPTPPQEATLVALLYSLVFTIAFLGLFELLYQKFENRHCQRGGLQ 177  
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